What is claimed is:

Sub a'

1. A variant human MLH1 or MSH2 ~~gene comprising hMLH1~~ mutant 1, ~~hMLH1 mutant~~ 2, hMSH2 mutant 1, hMSH2 mutant 2 or ~~hMSH2~~ mutant 3.

Sub B'

2. A method of diagnosing hereditary non-polyposis colorectal cancer in a patient comprising:

(a) obtaining a DNA sample from a patient; and

(b) screening the DNA sample for the variant human MLH1 or MSH2 gene of claim 1, wherein the presence of the variant gene is indicative of hereditary non-polyposis colorectal cancer.

3. A method for predicting susceptibility of a patient to developing hereditary non-polyposis colorectal cancer comprising:

(a) obtaining a DNA sample from a patient; and

(b) screening the DNA sample for the variant human MLH1 or MSH2 gene of claim 1, wherein the presence of the variant gene is indicative of a susceptibility to hereditary non-polyposis colorectal cancer.

4. A method of identifying mutants in splice donor or acceptor sites of a human MLH1 gene comprising sequencing splice donor or acceptor sites of the human MLH1 gene with intronic primers for the human MLH1 gene and analyzing the sequences to identify any mutants.

5. An intronic primer for human MLH1.

6. A method of identifying mutants in splice donor or acceptor sites of a human MSH2 gene, comprising sequencing splice donor or acceptor sites of the human MSH2 gene with intronic primers for the human MSH2 gene and analyzing the sequences to identify any mutants.

7. An intronic primer for human MSH2.

8. A transgenic model system for colorectal cancer comprising cells expressing the variant human MLH1 or MSH2 gene of claim 1.